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RAW SEQUENCE LISTING   DATE: 01/07/2002
PATENT APPLICATION: US/09/954,936   TIME: 14:47:57

Input Set : N:\Crf3\RULE60\09954936.raw
Output Set: N:\CRF3\01072002\I954936.raw

```
 1 <110> APPLICANT: Briggs, Clark A.
 2        Gopalakrishnan, Murali
 3        McKenna, David G.
 4        Monteggia, Lisa M.
 5        Roch, Jean-Marc
 6        Sullivan, James P.
 7        Touma, Edward
 8        Abbott Laboratories
 9 <120> TITLE OF INVENTION: A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE
10        RECEPTOR SUBUNIT, AND METHODS OF PRODUCTION AND USES THEREOF
11 <130> FILE REFERENCE: 6017.US.01
12 <140> CURRENT APPLICATION NUMBER: 09/954,936
13 <141> CURRENT FILING DATE: 2001-09-18
14 <150> PRIOR APPLICATION NUMBER: 08/771,737
15 <151> PRIOR FILING DATE: 1996-12-20
16 <160> NUMBER OF SEQ ID NOS: 8
17 <170> SOFTWARE: FastSEQ for Windows Version 3.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1590
21 <212> TYPE: DNA
22 <213> ORGANISM: homo sapien
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (9)...(1514)
26 <400> SEQUENCE: 1
27        tcgagccc atg agg tgt agc ccc gga gga gtg tgg ctg gca ctg gca gca      50
28                 Met Arg Cys Ser Pro Gly Gly Val Trp Leu Ala Leu Ala Ala
29                  1               5                  10
30        tct ctc ctg cac gtg tcc ctg caa ggc gag ttc cag agg aag ctt tac      98
31        Ser Leu Leu His Val Ser Leu Gln Gly Glu Phe Gln Arg Lys Leu Tyr
32         15              20                  25                  30
33        aag gag ctg gtc aag aac tac aat ccc ttg gag agg ccc gtg gcc aat     146
34        Lys Glu Leu Val Lys Asn Tyr Asn Pro Leu Glu Arg Pro Val Ala Asn
35                        35                  40                  45
36        gac tcg caa cca ctc acc gtc tac ttc tcc ctg agc ctc ctg cag atc     194
37        Asp Ser Gln Pro Leu Thr Val Tyr Phe Ser Leu Ser Leu Leu Gln Ile
38                    50                  55                  60
39        atg gac gtg gat gag aag aac caa gtt tta acc acc aac att tgg ctg     242
40        Met Asp Val Asp Glu Lys Asn Gln Val Leu Thr Thr Asn Ile Trp Leu
41                65                  70                  75
42        caa atg tct tgg aca gat cac tat tta cag tgg aat gtg tca gaa tat     290
43        Gln Met Ser Trp Thr Asp His Tyr Leu Gln Trp Asn Val Ser Glu Tyr
44            80                  85                  90
45        cca ggg gtg aag act gtt cgt ttc cca gat ggc cag att tgg aaa cca     338
46        Pro Gly Val Lys Thr Val Arg Phe Pro Asp Gly Gln Ile Trp Lys Pro
47         95                 100                 105                 110
48        gac att ctt ctc tat aac agt gct gat gag cgc ttt gac gcc aca ttc     386
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49      Asp Ile Leu Leu Tyr Asn Ser Ala Asp Glu Arg Phe Asp Ala Thr Phe
50                      115                 120                 125
51      cac act aac gtg ttg gtg aat tct tct ggg cat tgc cag tac ctg cct    434
52      His Thr Asn Val Leu Val Asn Ser Ser Gly His Cys Gln Tyr Leu Pro
53                      130                 135                 140
54      cca ggc ata ttc aag agt tcc tgc tac atc gat gta cgc tgg ttt ccc    482
55      Pro Gly Ile Phe Lys Ser Ser Cys Tyr Ile Asp Val Arg Trp Phe Pro
56                      145                 150                 155
57      ttt gat gtg cag cac tgc aaa ctg aag ttt ggg tcc tgg tct tac gga    530
58      Phe Asp Val Gln His Cys Lys Leu Lys Phe Gly Ser Trp Ser Tyr Gly
59                      160                 165                 170
60      ggc tgg tcc ttg gat ctg cag atg cag gag gca gat atc agt ggc tat    578
61      Gly Trp Ser Leu Asp Leu Gln Met Gln Glu Ala Asp Ile Ser Gly Tyr
62      175                 180                 185                 190
63      atc ccc aat gga gaa tgg gac cta gtg gga atc ccc ggc aag agg agt    626
64      Ile Pro Asn Gly Glu Trp Asp Leu Val Gly Ile Pro Gly Lys Arg Ser
65                      195                 200                 205
66      gaa agg ttc tat gag tgc tgc aaa gag ccc tac ccc gat gtc acc ttc    674
67      Glu Arg Phe Tyr Glu Cys Cys Lys Glu Pro Tyr Pro Asp Val Thr Phe
68                      210                 215                 220
69      aca gtg acc atg cgc cgc agg aca ctc tac tat ggc ctc aac ctg ctg    722
70      Thr Val Thr Met Arg Arg Arg Thr Leu Tyr Tyr Gly Leu Asn Leu Leu
71                      225                 230                 235
72      atc ccc tgt gtg ctc atc tcc gcc ctc gcc ctg ctg gtg ttc ctg ctt    770
73      Ile Pro Cys Val Leu Ile Ser Ala Leu Ala Leu Leu Val Phe Leu Leu
74                      240                 245                 250
75      cct gca gat tcc ggg gag aag att tcc ctg ggg ata aca gtc tta ctc    818
76      Pro Ala Asp Ser Gly Glu Lys Ile Ser Leu Gly Ile Thr Val Leu Leu
77      255                 260                 265                 270
78      tct ctt acc acc ttc atg ctg ctc gtg gct gag atc atg ccc gca aca    866
79      Ser Leu Thr Thr Phe Met Leu Leu Val Ala Glu Ile Met Pro Ala Thr
80                      275                 280                 285
81      tcc gat tcg gta cca ttg ata gcc cag tac ttc gcc agc acc atg atc    914
82      Ser Asp Ser Val Pro Leu Ile Ala Gln Tyr Phe Ala Ser Thr Met Ile
83                      290                 295                 300
84      atc gtg ggc ctc tcg gtg gtg gtg acg gtg atc gtg ctg cag tac cac    962
85      Ile Val Gly Leu Ser Val Val Val Thr Val Ile Val Leu Gln Tyr His
86                      305                 310                 315
87      cac cac gac ccc gac ggc ggc aag atg ccc aag tgg acc aga gtc atc   1010
88      His His Asp Pro Asp Gly Gly Lys Met Pro Lys Trp Thr Arg Val Ile
89                      320                 325                 330
90      ctt ctg aac tgg tgc gcg tgg ttc ctg cga atg aag agg ccc ggg gag   1058
91      Leu Leu Asn Trp Cys Ala Trp Phe Leu Arg Met Lys Arg Pro Gly Glu
92      335                 340                 345                 350
93      gac aag gtg cgc ccg gcc tgc cag cac aag cag cgg cgc tgc agc ctg   1106
94      Asp Lys Val Arg Pro Ala Cys Gln His Lys Gln Arg Arg Cys Ser Leu
95                      355                 360                 365
96      gcc agt gtg gag atg agc gcc gtg gcg ccg ccg ccc gcc agc aac ggg   1154
97      Ala Ser Val Glu Met Ser Ala Val Ala Pro Pro Pro Ala Ser Asn Gly
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 98              370             375             380
 99     aac ctg ctg tac atc ggc ttc cgc ggc ctg gac ggc gtg cac tgt gtc      1202
100     Asn Leu Leu Tyr Ile Gly Phe Arg Gly Leu Asp Gly Val His Cys Val
101             385             390             395
102     ccg acc ccc gac tct ggg gta gtg tgt ggc cgc atg gcc tgc tcc ccc      1250
103     Pro Thr Pro Asp Ser Gly Val Val Cys Gly Arg Met Ala Cys Ser Pro
104         400             405             410
105     acg cac gat gag cac ctc ctg cac ggc ggg caa ccc ccc gag ggg gac      1298
106     Thr His Asp Glu His Leu Leu His Gly Gly Gln Pro Pro Glu Gly Asp
107     415             420             425             430
108     ccg gac ttg gcc aag atc ctg gag gag gtc cgc tac att gcc aac cgc      1346
109     Pro Asp Leu Ala Lys Ile Leu Glu Glu Val Arg Tyr Ile Ala Asn Arg
110             435             440             445
111     ttc cgc tgc cag gac gaa agc gag gcg gtc tgc agc gag tgg aag ttc      1394
112     Phe Arg Cys Gln Asp Glu Ser Glu Ala Val Cys Ser Glu Trp Lys Phe
113             450             455             460
114     gcc gcc tgt gtg gtg gac cgc ctg tgc ctc atg gcc ttc tcg gtc ttc      1442
115     Ala Ala Cys Val Val Asp Arg Leu Cys Leu Met Ala Phe Ser Val Phe
116             465             470             475
117     acc atc atc tgc acc atc ggc atc ctg atg tcg gct ccc aac ttc gtg      1490
118     Thr Ile Ile Cys Thr Ile Gly Ile Leu Met Ser Ala Pro Asn Phe Val
119         480             485             490
120     gag gcc gtg tcc aaa gac ttt gcg taaccacgcc tggttctgta catgtggaaa      1544
121     Glu Ala Val Ser Lys Asp Phe Ala
122     495             500
123     actcacagat gggcaagcgc tttggcttgg cgagattcgg ccggaa                   1590
125 <210> SEQ ID NO: 2
126 <211> LENGTH: 502
127 <212> TYPE: PRT
128 <213> ORGANISM: homo sapien
129 <400> SEQUENCE: 2
130     Met Arg Cys Ser Pro Gly Gly Val Trp Leu Ala Leu Ala Ala Ser Leu
131      1               5               10              15
132     Leu His Val Ser Leu Gln Gly Glu Phe Gln Arg Lys Leu Tyr Lys Glu
133             20              25              30
134     Leu Val Lys Asn Tyr Asn Pro Leu Glu Arg Pro Val Ala Asn Asp Ser
135             35              40              45
136     Gln Pro Leu Thr Val Tyr Phe Ser Leu Ser Leu Leu Gln Ile Met Asp
137         50              55              60
138     Val Asp Glu Lys Asn Gln Val Leu Thr Thr Asn Ile Trp Leu Gln Met
139     65              70              75              80
140     Ser Trp Thr Asp His Tyr Leu Gln Trp Asn Val Ser Glu Tyr Pro Gly
141             85              90              95
142     Val Lys Thr Val Arg Phe Pro Asp Gly Gln Ile Trp Lys Pro Asp Ile
143             100             105             110
144     Leu Leu Tyr Asn Ser Ala Asp Glu Arg Phe Asp Ala Thr Phe His Thr
145             115             120             125
146     Asn Val Leu Val Asn Ser Ser Gly His Cys Gln Tyr Leu Pro Pro Gly
147         130             135             140
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```
148    Ile Phe Lys Ser Ser Cys Tyr Ile Asp Val Arg Trp Phe Pro Phe Asp
149    145                 150                 155                 160
150    Val Gln His Cys Lys Leu Lys Phe Gly Ser Trp Ser Tyr Gly Gly Trp
151                    165                 170                 175
152    Ser Leu Asp Leu Gln Met Gln Glu Ala Asp Ile Ser Gly Tyr Ile Pro
153                    180                 185                 190
154    Asn Gly Glu Trp Asp Leu Val Gly Ile Pro Gly Lys Arg Ser Glu Arg
155                195                 200                 205
156    Phe Tyr Glu Cys Cys Lys Glu Pro Tyr Pro Asp Val Thr Phe Thr Val
157                210                 215                 220
158    Thr Met Arg Arg Arg Thr Leu Tyr Tyr Gly Leu Asn Leu Leu Ile Pro
159    225                 230                 235                 240
160    Cys Val Leu Ile Ser Ala Leu Ala Leu Leu Val Phe Leu Leu Pro Ala
161                    245                 250                 255
162    Asp Ser Gly Glu Lys Ile Ser Leu Gly Ile Thr Val Leu Leu Ser Leu
163                    260                 265                 270
164    Thr Thr Phe Met Leu Leu Val Ala Glu Ile Met Pro Ala Thr Ser Asp
165                    275                 280                 285
166    Ser Val Pro Leu Ile Ala Gln Tyr Phe Ala Ser Thr Met Ile Ile Val
167                290                 295                 300
168    Gly Leu Ser Val Val Val Thr Val Ile Val Leu Gln Tyr His His His
169    305                 310                 315                 320
170    Asp Pro Asp Gly Gly Lys Met Pro Lys Trp Thr Arg Val Ile Leu Leu
171                    325                 330                 335
172    Asn Trp Cys Ala Trp Phe Leu Arg Met Lys Arg Pro Gly Glu Asp Lys
173                    340                 345                 350
174    Val Arg Pro Ala Cys Gln His Lys Gln Arg Arg Cys Ser Leu Ala Ser
175                    355                 360                 365
176    Val Glu Met Ser Ala Val Ala Pro Pro Pro Ala Ser Asn Gly Asn Leu
177                370                 375                 380
178    Leu Tyr Ile Gly Phe Arg Gly Leu Asp Gly Val His Cys Val Pro Thr
179    385                 390                 395                 400
180    Pro Asp Ser Gly Val Val Cys Gly Arg Met Ala Cys Ser Pro Thr His
181                    405                 410                 415
182    Asp Glu His Leu Leu His Gly Gly Gln Pro Pro Glu Gly Asp Pro Asp
183                    420                 425                 430
184    Leu Ala Lys Ile Leu Glu Glu Val Arg Tyr Ile Ala Asn Arg Phe Arg
185                435                 440                 445
186    Cys Gln Asp Glu Ser Glu Ala Val Cys Ser Glu Trp Lys Phe Ala Ala
187                450                 455                 460
188    Cys Val Val Asp Arg Leu Cys Leu Met Ala Phe Ser Val Phe Thr Ile
189    465                 470                 475                 480
190    Ile Cys Thr Ile Gly Ile Leu Met Ser Ala Pro Asn Phe Val Glu Ala
191                    485                 490                 495
192    Val Ser Lys Asp Phe Ala
193                    500
195 <210> SEQ ID NO: 3
196 <211> LENGTH: 20
197 <212> TYPE: DNA
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RAW SEQUENCE LISTING   DATE: 01/07/2002
PATENT APPLICATION: US/09/954,936   TIME: 14:47:58

Input Set : N:\Crf3\RULE60\09954936.raw
Output Set: N:\CRF3\01072002\I954936.raw

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198 <213> ORGANISM: Homo Sapien
199 <400> SEQUENCE: 3
200      gtttgggtcc tggtcttacg                                    20
202 <210> SEQ ID NO: 4
203 <211> LENGTH: 23
204 <212> TYPE: DNA
205 <213> ORGANISM: Homo Sapien
206 <400> SEQUENCE: 4
207      gcagcatgaa ggtggtaaga gag                                23
209 <210> SEQ ID NO: 5
210 <211> LENGTH: 23
211 <212> TYPE: DNA
212 <213> ORGANISM: Homo Sapien
213 <400> SEQUENCE: 5
214      ctctcttacc accttcatgc tgc                                23
216 <210> SEQ ID NO: 6
217 <211> LENGTH: 20
218 <212> TYPE: DNA
219 <213> ORGANISM: Homo Sapien
220 <400> SEQUENCE: 6
221      gtactgcagc acgatcaccg                                    20
223 <210> SEQ ID NO: 7
224 <211> LENGTH: 20
225 <212> TYPE: DNA
226 <213> ORGANISM: Homo Sapein
227 <400> SEQUENCE: 7
228      cgagcccatg aggtgtagcc                                    20
230 <210> SEQ ID NO: 8
231 <211> LENGTH: 20
232 <212> TYPE: DNA
233 <213> ORGANISM: Homo Sapien
234 <400> SEQUENCE: 8
235      ccaggcattc ggagcttgcc                                    20
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VERIFICATION SUMMARY   DATE: 01/07/2002
PATENT APPLICATION: **US/09/954,936**   TIME: 14:47:59

Input Set : **N:\Crf3\RULE60\09954936.raw**
Output Set: **N:\CRF3\01072002\I954936.raw**